GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 2, 2002, 18:03:43 ; Search time 20.94 Seconds
(without alignments)
1670.321 Million cell updates/sec

Title: US-09-886-400-4
Perfect score: 1877
Sequence: 1 LRALVFHGNLQYAEIPKSEI.....RRLDAFRAIYNDWRGENGEP 364

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1494	79.6	364	2	E71144	hypothetical prote
2	169	9.0	529	2	AC2112	hypothetical prote
3	162.5	8.7	529	2	S76831	hypothetical prote
4	161.5	8.6	633	2	G71241	probable alpha-amy
5	157.5	8.4	686	1	ALDYAT	amylase A (EC 3.2.
6	147	7.8	527	2	F97197	uncharacterized co
7	145.5	7.8	655	2	E75206	alpha-amylase (or
8	141.5	7.5	467	2	B64501	alpha-amylase (EC
9	141.5	7.5	649	2	A49512	alpha-amylase (EC
10	130.5	7.0	560	2	D71011	hypothetical prote
11	128	6.8	923	2	G83826	hypothetical prote
12	124	6.6	1362	2	A75207	amylopullulanase P
13	123.5	6.6	744	2	AC1970	hypothetical prote
14	120.5	6.4	324	1	B69553	methanol dehydroge
15	119	6.3	602	2	C75120	hypothetical prote
16	113	6.0	1069	2	AF1930	hypothetical prote
17	112	6.0	312	2	I40383	malate dehydrogena
18	111	5.9	526	2	D71334	conserved hypothet
19	109.5	5.8	447	2	E90250	alpha amylase [imp
20	106	5.6	526	2	B70859	hypothetical prote
21	105.5	5.6	902	2	E90270	conserved hypothet
22	104	5.5	704	2	G96587	hypothetical prote
23	103.5	5.5	314	2	F84044	malate dehydrogena
24	101.5	5.4	705	2	F70475	VacB protein (ribo
25	100.5	5.4	266	2	G96943	probable xylanase/
26	100.5	5.4	619	2	D71361	probable alpha-amy
27	99	5.3	4845	2	T31067	BIR repeat contain
28	98.5	5.2	588	2	AE1926	two-component resp
29	98	5.2	503	2	T19319	hypothetical prote
30	98	5.2	764	1	H70414	conserved hypothet
31	97.5	5.2	402	2	T14710	probable transposa
32	97.5	5.2	402	2	AB0193	transposase, IS285
33	97.5	5.2	402	2	AB0358	transposase, IS285
34	97.5	5.2	402	2	AB0472	transposase, IS285
35	97.5	5.2	402	2	AC0341	transposase, IS285
36	97.5	5.2	402	2	AD0002	transposase, IS285
37	97.5	5.2	402	2	AE0190	transposase, IS285
38	97.5	5.2	402	2	AE0242	transposase, IS285
39	97.5	5.2	402	2	AE0267	transposase, IS285
40	97.5	5.2	402	2	AF0348	transposase, IS285
41	97.5	5.2	402	2	AG0210	transposase, IS285
42	97.5	5.2	402	2	AG0260	transposase, IS285
43	97.5	5.2	402	2	AG0264	transposase, IS285
44	97.5	5.2	402	2	AG0339	transposase, IS285
45	97.5	5.2	402	2	AH0193	transposase, IS285

ALIGNMENTS

RESULT 1
E71144
hypothetical protein PH0368 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 08-Sep-2000
C;Accession: E71144
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
A;Accession: E71144
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-364 <KAW>
A;Cross-references: GB:AP000002; NID:g3236129; PIDN:BAA29442.1; PID:d1030385; PID:g32
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
A;Gene: PH0368
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0368

Query Match 79.6%; Score 1494; DB 2; Length 364;
Best Local Similarity 75.8%; Pred. No. 2.7e-105;
Matches 275; Conservative 49; Mismatches 39; Indels 0; Gaps 0;

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Qy       1 LRALVFHGNLQYAEIPKSEIPKVIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIID 60
           :|||:|||||||||||||| || |||||:| | |  ||| ||||||||||:|:|||:::|
Db       1 MRALIFHGNLQYAEIPKHEISKVIEKSYFPTISELIKREIPFGLNITGYSLQFLPQELIH 60

Qy      61 LVKGGIASDLIEIIGTSYTHAILPLLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY 120
           |:| || |:||||:|||||||||||| |||:|||::||||:|||:||:|| |||||||||
Db      61 LIKEGIESELIEILGTSYTHAILPLLTLSRIEAQIKRDREIKEEIFEVSPGGFWLPELAY 120

Qy     121 DPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPLYPHLIKAQREKRFRYISYLLG 180
           |||||||||:|| |||||||||||||| ||||||| ||||||:|||||| : | |::|||||
Db     121 DPIIPAILRDNEYEYLFADGEAMLFSNHLNSAIKSIKPLYPYLIKAQRGEGFVYLNYLLG 180

Qy     181 LRELRKAIKLVFEGKVTLKAVKDIEAVPVWVAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240
           ||||:||| | | |||||:|||||||:||||::| |:||| || |||:||:||::||: ||
Db     181 LRELKKAINLTFGGKVTLEAVKDIEAIPVWVSINIAIMLGAGRFPLMSPKRVANWIKGKD 240

Qy     241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
           |||||||||:||| |||:::::: ||:||::||  ||||| :::|:|| ||||||||||
Db     241 EILLYGTDIEFLGYRSIAGHKIAISGLMEVLNELGGELCLPRDIRHNGRRLYLRTSSWAP 300

Qy     301 DKSLRIWREDEGNARLNMLSYNMRGELALLAENSDARGWEPLPERRLDAFRAIYNDWRGE 360
           |||||||:|||||||||||:| | || | |||||||||||||||||||||||||| || |
Db     301 DKSLRIWKEDEGNARLNMLTYCMDGEFAFLAENSDARGWEPLPERRLDAFKAIYKYWRNE 360

Qy     361 NGE 363
```

```
          ||:
Db    361 NGK 363


RESULT   2
AC2112
hypothetical protein alr2450 [imported] - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C;Accession: AC2112
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74149.1; PID:g17131542; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2450
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1386


  Query Match             9.0%;  Score 169;  DB 2;  Length 529;
  Best Local Similarity   21.0%;  Pred. No. 5.6e-05;
  Matches  104;  Conservative   55;  Mismatches  162;  Indels  174;  Gaps   21;

Qy       3 ALVFHGNLQYAEIPKSE-------IPKVIEKAYIP---VIETLIKEEIPFGL-------- 44
           ||| | :| :   |:|:       : : | : |||   | : | :: | | :
Db       7 ALVLHAHLPFVRHPESDYVLEEEWLYEAITETYIPLLKVFDGLKRDGIDFKITMSMTPPL 66

Qy      45 ------------------------------NITGYTLKFLPK------------------ 56
                                          |    |::| :
Db      67 VSMLRDPLLQERYDAHLAQLEELIELEGERNAQNGHLRYLAEHYATEFNEARQMWERYNG 126

Qy      57 DIIDLVKGGIASDLIEIIGTSYTHAILPLLPL--SRVEAQVQRDREVKEELFELSPKGFW 114
           |::   |    |: :|||    ||  |||: :    | ||:|   |  || |   ||| |
Db     127 DLVTAFKQFQDSNNLEIITCGATHGYLPLMKMYPQAVWAQIQVACEHYEETFGRPPKGIW 186

Qy     115 LPELAYDPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPL--------------- 159
           ||| ||   :  :| | |  |   ||  :|: |          |:
Db     187 LPECAYYEGLERMLADAGLRYFLTDGHGILY-ARPRPRFGTYAPIFTETGVAAFGRDHES 245

Qy     160 ----------YPHLIKAQR-------EKRFRYISYLLGLRELRKAIKLVFEGKVT----- 197
                     ||   : :         |  : ||   :     ||   : :  |:|
Db     246 SQQVWSSEVGYPGAAEYREFYKDLGWEAEYEYIKPYIMPNGQRKNTGIKYH-KITGRGLG 304

Qy     198 --LKAVKDIEAVPVWVAVNTAVMLGIGRLPLMNPKKVASWIEDKDNIL--LYGT------ 247
             ||: |    | |      |              :  |::: :::     |||
Db     305 LSDKALYD----PYWAKEKAA-------------EHAANFMYNRERQAEHLYGIMQRPPI 347

Qy     248 -----DIEFIGYRDIAG------------YRMSVEGLLEVIDELNSE----LCLPSELKH 286
                | |  |:    |            |       :  : | | :|    :| ||:
Db     348 IVSPYDAELFGHWWYEGPWFIDYLFRKSWYDQGTYAMTHLADYLRNEPTQQVCRPSQ--- 404

Qy     287 SGRELYLRTSSWAPDKSLRIWREDEGNA----RLNMLSYNMRGELALLAENSDARGWEPL 342
                   |||        |  :| ||      |:  :  |  |:: | |  |  ||  |
Db     405 ---------SSWGYKGFHEYWL-NETNAWIYPHLHKAAERMI-EISTL-EPEDELGWRAL 452

Qy     343 PERRLDAFRAIYNDW 357
           :   :   |  :||
Db     453 NQAARELLLAQSSDW 467


RESULT   3
S76831
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76831
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A;Reference number: S74322; MUID:97061201
A;Accession: S76831
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <KAN>
A;Cross-references: EMBL:D90916; GB:AB001339; NID:g1653715; PIDN:BAA18743.1; PID:g165
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1386


  Query Match             8.7%;  Score 162.5;  DB 2;  Length 529;
  Best Local Similarity   21.4%;  Pred. No. 0.00017;
  Matches  101;  Conservative   47;  Mismatches  140;  Indels  183;  Gaps   19;

Qy       3 ALVFHGNLQYAEIPKSE-------IPKVIEKAYIPVI---ETLIKEEIPFGLNIT----- 47
           ||| | :| :   |:|:       : : | : |||:|   | | :: : | : ::
Db       7 ALVLHAHLPFVRHPESDYVLEEEWLYEAITETYIPLIHVFEGLKRDGVDFKITMSMTPPL 66

Qy      48 ------------------------------------GYTLKFLPK-------------- 56
                                                |   |  |
Db      67 VSMLRDPLLQQRYEAHLSLLQELLAKEIVRNEHNGHLQYLADFYAKEFAAIRETWERYDG 126

Qy      57 DIIDLVKGGIASDLIEIIGTSYTHAILPLLPL--SRVEAQVQRDREVKEELFELSPKGFW 114
           |::   |    |: :|||    ||   ||: :    | ||::   |  || |  |||| |
Db     127 DLVTAFKQFQDSNNLEIITCGATHGYFPLMKMYPQAVWAQIKVACEHYEENFGRSPKGIW 186

Qy     115 LPELAYDPIIPAILKDNGYEYLFADGEAMLFSA-----------------------HLNS 151
           ||| ||   :  :| | |  |   ||  :|::                        | :|
Db     187 LPECAYYEGVERMLADAGLRYFLVDGHGILYARPRPKFGTYAPIFTETGVAAFGRDHESS 246

Qy     152 -------AIKPIKPLYPHLIK-AQREKRFRYISYLLGLRELRKAIKLVF------EGKVT 197
                  |  |:|    |    |  : ||   :     || | : :       :| ::
Db     247 QQVWSSQVGYPGDPVYREFYKDLGWEAEYEYIKPYIMPNGQRKNIGIKYHKITSRDGGLS 306

Qy     198 LKAVKDIEAVPVWVAVNTAV---------------MLGI-GRLPLMNPKKVAS-----WI 236
           ||  |    | |    |                  : || || ||:     |       |
Db     307 EKAWYD----PYWAKEKAAEHASNFMYNRQQQVGHLSGIMGRPPLVVSPYDAELFGHWWY 362

Qy     237 E--------------DKDNI-------LLYGTDIEFI--------GYRDIAGY------- 260
           |              |:|          | |   : :         ||:    |
Db     363 EGPWFIDYLFRKSWFDQDTFEMTHLADYLRGNPHQQVCRPSQSSWGYKGFHEYWLNDTNA 422

Qy     261 -----------RMSVEGLLEVIDELNSELCLPSELKHSGRELYL-RTSSWA 299
                      ||       | :|||  :      |  : ||| | ::| ||
Db     423 WIYPHLHKAAERMIELSHREAVDELEEK-----ALNQAARELLLAQSSDWA 468


RESULT   4
G71241
probable alpha-amylase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: G71241
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
A;Accession: G71241
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-633 <KAW>
A;Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29262.1; PID:g3256579
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
C;Genetics:
```

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Qy       1 LRALVFHGNLQYAEIPKSEIPKVIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIID 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 LRALVFHGNLQYAEIPKSEIPKVIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIID 60

Qy      61 LVKGGIASDLIEIIGTSYTHAILPLLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVKGGIASDLIEIIGTSYTHAILPLLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY 120

Qy     121 DPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPLYPHLIKAQREKRFRYISYLLG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 DPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPLYPHLIKAQREKRFRYISYLLG 180

Qy     181 LRELRKAIKLVFEGKVTLKAVKDIEAVPVWVAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 LRELRKAIKLVFEGKVTLKAVKDIEAVPVWVAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240

Qy     241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300

Qy     301 DKSLRIWREDEGNARLNMLSYNMRGELALLAENSDARGWEPLPERRLDAFRAIYNDWRGE 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 DKSLRIWREDEGNARLNMLSYNMRGELALLAENSDARGWEPLPERRLDAFRAIYNDWRGE 360

Qy     361 NGEP 364
           ||||
Db     361 NGEP 364
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```
RESULT  2
US-09-407-806-4
; Sequence 4, Application US/09407806
;  GENERAL INFORMATION:
;     APPLICANT:  Murphy, Dennis
;     APPLICANT:  Reid, John
;     TITLE OF INVENTION:  ALPHA-GALACTOSIDASE
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  4225 Executive Square, Suite 1400
;       CITY:  La Jolla
;       STATE:  CA
;       COUNTRY:  US
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/407,806
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/613,220
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haile, Ph.D., Lisa A.
;       REGISTRATION NUMBER:  38,347
;       REFERENCE/DOCKET NUMBER:  09010/004001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-678-5070
;       TELEFAX:  619-68-5099
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  346 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FRAGMENT TYPE:  internal
US-09-407-806-4
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  Query Match             84.2%;  Score 1580;  DB 18;  Length 346;
  Best Local Similarity   94.5%;  Pred. No. 3.4e-152;
  Matches  344;  Conservative    1;  Mismatches    1;  Indels   18;  Gaps   18;

Qy       1 LRALVFHGNLQYAEIPKSEIPKVIEKAYIPVIETLIKEEIPFGLNITGYTLKFLPKDIID 60
           |||||||||||||||||| |||||||||||||||| |||||||||||||||||||||||||
Db       1 LRALVFHGNLQYAEIPKSE-PKVIEKAYIPVIETLIKEE-PFGLNITGYTLKFLPKDII- 57

Qy      61 LVKGGIASDLIEIIGTSYTHAILPLLPLSRVEAQVQRDREVKEELFELSPKGFWLPELAY 120
           |||||||||||||||||| |||||||||||||||| ||||||:||||||||||
Db      58 LVKGGIASDLIEIIGTSYT-AILPLLPLSRVEAQVQRDR-VKEELFEVSPKGFWLPELA- 114

Qy     121 DPIIPAILKDNGYEYLFADGEAMLFSAHLNSAIKPIKPLYPHLIKAQREKRFRYISYLLG 180
           |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Db     115 DPIIPAILKDNGYEYLFAD-EAMLFSAHLNSAIKPIKPL-PHLIKAQREKRFRYISYLL- 171

Qy     181 LRELRKAIKLVFEGKVTLKAVKDIEAVPVWVAVNTAVMLGIGRLPLMNPKKVASWIEDKD 240
           |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Db     172 LRELRKAIKLVFEGKVTLK-VKDIEAVPVWVAVNTAVML-IGRLPLMNPKKVASWIEDK- 228

Qy     241 NILLYGTDIEFIGYRDIAGYRMSVEGLLEVIDELNSELCLPSELKHSGRELYLRTSSWAP 300
           |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Db     229 NILLYGTDIEFIGYRDIAG-RMSVEGLLEVIDELNSELC-PSELKHSGRELYLRTSSWA- 285

Qy     301 DKSLRIWREDEGNARLNMLSYNMRGELALLAENSDARGWEPLPERRLDAFRAIYNDWRGE 360
           |||||||||||||||||| |||||||| ||||||||| ||||||||||||||||||||
Db     286 DKSLRIWREDEGNARLNML-YNMRGELAFLAENSDARGW-PLPERRLDAFRAIYNDWRG- 342

Qy     361 NGEP 364
           ||||
Db     343 NGEP 346
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RESULT  3
US-09-407-806A-4
; Sequence 4, Application US/09407806A
;  GENERAL INFORMATION:
;     APPLICANT:  Murphy, Dennis
;     APPLICANT:  Reid, John
;     TITLE OF INVENTION:  ALPHA-GALACTOSIDASE
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Richardson, P.C.
;       STREET:  4225 Executive Square, Suite 1400
;       CITY:  La Jolla
;       STATE:  CA
;       COUNTRY:  US
;       ZIP:  92037
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  Windows95
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/407,806A
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/613,220
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haile, Ph.D., Lisa A.
;       REGISTRATION NUMBER:  38,347
;       REFERENCE/DOCKET NUMBER:  09010/004001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  619-678-5070
;       TELEFAX:  619-68-5099
;       TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  346 amino acids
;       TYPE:  amino acid
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